

What is claimed is:

1. A system for searching for relationships between base sequences in genes, comprising:

a theoretical value calculating portion which calculates theoretical restriction fragment length values of known genes digested by restriction enzymes based on restriction enzyme data in which kinds of restriction enzymes, recognition sites recognized by the restriction enzymes, and restriction sites at which the restriction enzymes cut in the recognition sites are stored in a related manner, and base sequence data in which kinds of known genes and base sequences of the known genes are stored in a related manner, and outputs theoretical restriction fragment patterns in which the kinds of known genes, the kinds of restriction enzymes, and the theoretical restriction fragment length values are stored in a related manner, and

a comparing portion which compares the theoretical restriction fragment patterns with measured restriction fragment patterns in which the kinds of restriction enzymes and measured restriction fragment length values obtained as a result of digesting a sample by the restriction enzymes followed by measurement are stored in a related manner, calculates the degree of similarity of the known genes to the sample, and outputs the degree of similarity as analysis result data.

2. A system for searching for relationships between base sequences as claimed in claim 1, further comprising a displaying portion that diagrammatically displays samples having a high degree of similarity therebetween or displays a known gene and a sample having a high degree of similarity therebetween in a related manner based on the analysis result data.

3. A system for searching for relationships between base sequences as claimed in claim 2, wherein said displaying portion displays samples having a high degree of similarity therebetween or displays a known gene and a sample having a high degree of similarity therebetween in a related manner by a dendrogram.

4. A system for searching for relationships between base sequences as claimed in claim 1, wherein said comparing portion calculates the degree of similarity based on the theoretical restriction fragment patterns and the measured restriction fragment patterns by using an unweighted-pair-group method with arithmetic mean.

5. A system for searching for relationships between base sequences as claimed in claim 1, further comprising an amplified sequence recognizing portion which reads pre-amplification base sequence data, and which produces post-amplification base sequence data based on primer data including recognition site data of primers used for the amplification,

wherein said theoretical value calculating portion calculates the theoretical restriction fragment length values based on the post-amplification base sequence data.

6. A method of searching for relationships between base sequence in genes, comprising:

a theoretical value calculating step for calculating theoretical restriction fragment length values of known genes digested by restriction enzymes based on restriction enzyme data in which kinds of restriction enzymes, recognition sites recognized by the restriction enzymes, and restriction sites at which the restriction enzymes cut in the recognition sites

are stored in a related manner, and base sequence data in which kinds of known genes and base sequences of the known genes are stored in a related manner, and outputting theoretical restriction fragment patterns in which the kinds of known genes, the kinds of restriction enzymes, and the theoretical restriction fragment length values are stored in a related manner, and

a comparing step for comparing the theoretical restriction fragment patterns with measured restriction fragment patterns in which the kinds of restriction enzymes and measured restriction fragment length values obtained as a result of digesting a sample by the restriction enzymes followed by measurement are stored in a related manner, calculating the degree of similarity of the known genes to the sample, and outputting it as analysis result data.

7. A method for searching for relationships between base sequences as claimed in claim 6, further comprising a displaying step for diagrammatically displaying samples having a high degree of similarity therebetween or a known gene and a sample having a high degree of similarity therebetween in a related manner based on the analysis result data.

8. A method for searching for relationships between base sequences as claimed in claim 7, wherein said displaying step displays samples having a high degree of similarity therebetween or displays a known gene and a sample having a high degree of similarity therebetween in a related manner by a dendrogram.

9. A method for searching for relationships between base sequences as claimed in claim 6, wherein said comparing step calculates the degree of similarity based on the

theoretical restriction fragment patterns and the measured restriction fragment patterns by using an unweighted-pair-group method with arithmetic mean.

10. A method for searching for relationships between base sequences as claimed in claim 6, further comprising an amplified sequence recognizing step for reading pre-amplification base sequence data, and producing post-amplification base sequence data based on primer data including recognition site data of the primers,

wherein said theoretical value calculating step calculates the theoretical restriction fragment length values based on the post-amplification base sequence data.

11. A recording medium readable on a computer having recorded therein a computer program for implementing:

a theoretical value calculating step for calculating theoretical restriction fragment length values of known genes digested by restriction enzymes based on restriction enzyme data in which kinds of restriction enzymes, recognition sites recognized by the restriction enzymes, and restriction sites at which the restriction enzymes cut in the recognition sites are stored in a related manner, and base sequence data in which kinds of known genes and base sequences of the known genes are stored in a related manner, and outputting theoretical restriction fragment patterns in which the kinds of known genes, the kinds of restriction enzymes, and theoretical restriction fragment length values are stored in a related manner, and

a comparing step for comparing the theoretical restriction fragment patterns with measured restriction fragment patterns in which the kinds of restriction enzymes and measured restriction fragment length values obtained as a result of digesting a sample by the restriction enzymes followed by measurement are stored in a related manner,

calculating the degree of similarity of the known genes to the sample, and outputting it as analysis result data.

12. A recording medium readable on a computer as claimed in claim 11, further having recorded therein a computer program for implementing a displaying step for diagrammatically displaying samples having a high degree of similarity therebetween or diagrammatically displaying a known gene and a sample having a high degree of similarity therebetween in a related manner based on the analysis result data.

13. A recording medium readable on a computer as claimed in claim 12, wherein said displaying step displays samples having a high degree of similarity therebetween or display a known gene and a sample having a high degree of similarity therebetween in a related manner by a dendrogram.

14. A recording medium readable on a computer as claimed in claim 11, wherein said comparing step calculates the degree of similarity based on the theoretical restriction fragment patterns and the measured restriction fragment patterns by using an unweighted-pair-group method with arithmetic mean.

15. A recording medium readable on a computer as claimed in claim 11, further having recorded therein a computer program for implementing an amplified sequence recognizing step for reading pre-amplification base sequence data, and producing post-amplification base sequence data by the primer based on primer data including a recognition site data of primers used for the amplification,

wherein said theoretical value calculating step calculates the theoretical

restriction fragment length values based on the post-amplification base sequence data.

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